

SEQUENCE LISTING

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SPRING, PAUL

<120> METHODS AND COMPOSITIONS OF A NOVEL SERINE PROTEASE

<130> UTSC:631USD1

<140> UNKNOWN
<141> 2004-01-28

<150> 09/653,464
<151> 2000-08-31

<150> 60/151,776
<151> 1999-08-31

<160> 21

<170> PatentIn Ver. 2.0

<210> 1
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<212> DNA
<213> Human

<400> 1

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Gly Ile Leu Thr Ala Ile Gly Met Val Leu Leu Gly Thr Arg Gly Ala
35 40 45

Thr Ala Ser Gln Leu Glu Glu Val Phe His Ser Glu Lys Glu Thr Lys
50 55 60

Ser Ser Arg Ile Lys Ala Glu Glu Lys Glu Val Ile Glu Asn Thr Glu
65 70 75 80

Ala Val His Gln Gln Phe Gln Lys Phe Leu Thr Glu Ile Ser Lys Leu
85 90 95

Thr Asn Asp Tyr Glu Leu Asn Ile Thr Asn Arg Leu Phe Gly Glu Lys
100 105 110

Thr Tyr Leu Phe Leu Gln Lys Tyr Leu Asp Tyr Val Glu Lys Tyr Tyr
115 120 125

His Ala Ser Leu Glu Pro Val Asp Phe Val Asn Ala Ala Asp Glu Ser
130 135 140

Arg Lys Lys Ile Asn Ser Trp Val Glu Ser Lys Thr Asn Glu Lys Ile
145 150 155 160

Lys Asp Leu Phe Pro Asp Gly Ser Ile Ser Ser Ser Thr Lys Leu Val
165 170 175

Leu Val Asn Met Val Tyr Phe Lys Gly Gln Trp Asp Arg Glu Phe Lys
180 185 190

Lys Glu Asn Thr Lys Glu Glu Lys Phe Trp Met Asn Lys Ser Thr Ser
195 200 205

Lys Ser Val Gln Met Met Thr Gln Ser His Ser Phe Ser Phe Thr Phe
210 215 220

Leu Glu Asp Leu Gln Ala Lys Ile Leu Gly Ile Pro Tyr Lys Asn Asn
225 230 235 240

Asp Leu Ser Met Phe Val Leu Leu Pro Asn Asp Ile Asp Gly Leu Glu
245 250 255

Lys Ile Ile Asp Lys Ile Ser Pro Glu Lys Leu Val Glu Trp Thr Ser
260 265 270

Pro Gly His Met Glu Glu Arg Lys Val Asn Leu His Leu Pro Arg Phe
275 280 285

Glu Val Glu Asp Ser Tyr Asp Leu Glu Ala Val Leu Ala Ala Met Gly
290 295 300

Met Gly Asp Ala Phe Ser Glu His Lys Ala Asp Tyr Ser Gly Met Ser
305 310 315 320

Ser Gly Ser Gly Leu Tyr Ala Gln Lys Phe Leu His Ser Ser Phe Val
325 330 335

Ala Val Thr Glu Glu Gly Thr Glu Ala Ala Ala Ala Thr Gly Ile Gly
340 345 350

Phe Thr Val Thr Ser Ala Pro Gly His Glu Asn Val His Cys Asn His
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370 375 380

Phe Gly Arg Phe Ser Ser Pro
385 390

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Ser Ser Pro Thr Ser Thr
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Leu Ser Ser Pro Ser Thr
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Arg Thr Gly His Gly Gly
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Gly Ile Leu Thr Ala Ile Gly Met Val Leu Leu Gly Thr Arg Gly Ala
35 40 45

Thr Ala Ser Gln Leu Glu Glu Val Phe His Ser Glu Lys Glu Thr Lys
50 55 60

Ser Ser Arg Ile Lys Ala Glu Glu Lys Glu Val Val Arg Ile Lys Ala
65 70 75 80

Glu Gly Lys Glu Ile Glu Asn Thr Glu Ala Val His Gln Gln Phe Gln
85 90 95

Lys Phe Leu Thr Glu Ile Ser Lys Leu Thr Asn Asp Tyr Glu Leu Asn
100 105 110

Ile Thr Asn Arg Leu Phe Gly Glu Lys Thr Tyr Leu Phe Leu Gln Lys
115 120 125

Tyr Leu Asp Tyr Val Glu Lys Tyr Tyr His Ala Ser Leu Glu Pro Val
130 135 140

Asp Phe Val Asn Ala Ala Asp Glu Ser Arg Lys Lys Ile Asn Ser Trp
145 150 155 160

Val Glu Ser Lys Thr Asn Glu Lys Ile Lys Asp Leu Phe Pro Asp Gly
165 170 175

Ser Ile Ser Ser Ser Thr Lys Leu Val Leu Val Asn Met Val Tyr Phe

180	185	190
Lys Gly Gln Trp Asp Arg Glu Phe Lys Lys Glu Asn Thr Lys Glu Glu		
195	200	205
Lys Phe Trp Met Asn Lys Ser Thr Ser Lys Ser Val Gln Met Met Thr		
210	215	220
Gln Ser His Ser Phe Ser Phe Thr Phe Leu Glu Asp Leu Gln Ala Lys		
225	230	235
Ile Leu Gly Ile Pro Tyr Lys Asn Asn Asp Leu Ser Met Phe Val Leu		
245	250	255
Leu Pro Asn Asp Ile Asp Gly Leu Glu Lys Ile Ile Asp Lys Ile Ser		
260	265	270
Pro Glu Lys Leu Val Glu Trp Thr Ser Pro Gly His Met Glu Glu Arg		
275	280	285
Lys Val Asn Leu His Leu Pro Arg Phe Glu Val Glu Asp Ser Tyr Asp		
290	295	300
Leu Glu Ala Val Leu Ala Ala Met Gly Met Gly Asp Ala Phe Ser Glu		
305	310	315
320		
His Arg Ala Asp Tyr Ser Gly Met Ser Ser Gly Ser Gly Leu Tyr Ala		
325	330	335
Gln Lys Phe Leu His Ser Ser Phe Val Ala Val Thr Glu Glu Gly Thr		
340	345	350
Glu Ala Ala Ala Ala Thr Gly Ile Gly Phe Thr Val Thr Ser Ala Leu		
355	360	365
Gly His Glu Asn Val His Cys Asn His Pro Phe Leu Phe Phe Ile Arg		
370	375	380
His Asn Glu Ser Asn Ser Ile Leu Phe Phe Gly Arg Phe Ser Ser Pro		
385	390	395
400		

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<213> Human

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Asp Leu Ser Met Phe Val Leu Leu Pro Asn Asp Ile Asp Gly Leu Glu
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Lys Val Asn Ala Tyr Thr Ser Leu Phe Phe Leu Ser Phe Pro Lys Ala
 35 40 45

 Phe Cys Leu Arg Ala Ser Glu
 50 55

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 Gln Gln Phe Arg Lys Ser Lys Glu Asn Asn Ile Phe Tyr Ser Pro Ile
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 Ser Ile Thr Ser Ala Leu Gly Met Val Leu Leu Gly Ala Lys Asp Asn
 35 40 45

 Thr Ala Gln Gln Ile Lys Lys Val Leu His Phe Asp Gln Val Thr Glu
 50 55 60

 Asn Thr Thr Gly Lys Ala Ala Thr Tyr His Val Asp Arg Ser Gly Asn
 65 70 75 80

 Val His His Gln Phe Gln Lys Leu Leu Thr Glu Phe Asn Lys Ser Thr
 85 90 95

 Asp Ala Tyr Glu Leu Lys Ile Ala Asn Lys Leu Phe Gly Glu Lys Thr
 100 105 110

 Tyr Leu Phe Leu Gln Glu Tyr Leu Asp Ala Ile Lys Lys Phe Tyr Gln
 115 120 125

 Thr Ser Val Glu Ser Val Asp Phe Ala Asn Ala Pro Glu Glu Ser Arg
 130 135 140

 Lys Lys Ile Asn Ser Trp Val Glu Ser Gln Thr Asn Glu Lys Ile Lys
 145 150 155 160

 Asn Leu Ile Pro Glu Gly Asn Ile Gly Ser Asn Thr Thr Leu Val Leu
 165 170 175

 Val Asn Ala Ile Tyr Phe Lys Gly Gln Trp Glu Lys Lys Phe Asn Lys
 180 185 190

 Glu Asp Thr Lys Glu Glu Lys Phe Trp Pro Asn Lys Asn Thr Tyr Lys
 195 200 205

 Ser Ile Gln Met Met Arg Gln Tyr Thr Ser Phe His Phe Ala Ser Leu
 210 215 220

 Glu Asp Val Gln Ala Lys Val Leu Glu Ile Pro Tyr Lys Gly Lys Asp
 225 230 235 240

Leu Ser Met Ile Val Leu Leu Pro Asn Glu Ile Asp Gly Leu Gln Lys
245 250 255

Leu Glu Glu Lys Leu Thr Ala Glu Lys Leu Met Glu Trp Thr Ser Leu
260 265 270

Gln Asn Met Arg Glu Thr Arg Val Asp Leu His Leu Pro Arg Phe Lys
275 280 285

Val Glu Glu Ser Tyr Asp Leu Lys Asp Thr Leu Arg Thr Met Gly Met
290 295 300

Val Asp Ile Phe Asn Gly Asp Ala Asp Leu Ser Gly Met Thr Gly Ser
305 310 315 320

Arg Gly Leu Val Leu Ser Gly Val Leu His Lys Ala Phe Val Glu Val
325 330 335

Thr Glu Glu Gly Ala Glu Ala Ala Ala Thr Ala Val Val Gly Phe
340 345 350

Gly Ser Ser Pro Thr Ser Thr Asn Glu Glu Phe His Cys Asn His Pro
355 360 365

Phe Leu Phe Phe Ile Arg Gln Asn Lys Thr Asn Ser Ile Leu Phe Tyr
370 375 380

Gly Arg Phe Ser Ser Pro
385 390

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<211> 390

<212> PRT

<213> Human

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Gln Gln Phe Arg Lys Ser Lys Glu Asn Asn Ile Phe Tyr Ser Pro Ile
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Ser Ile Thr Ser Ala Leu Gly Met Val Leu Leu Gly Ala Lys Asp Asn
35 40 45

Thr Ala Gln Gln Ile Ser Lys Val Leu His Phe Asp Gln Val Thr Glu
50 55 60

Asn Thr Thr Glu Lys Ala Ala Thr Tyr His Val Asp Arg Ser Gly Asn
65 70 75 80

Val His His Gln Phe Gln Lys Leu Leu Thr Glu Phe Asn Lys Ser Thr
85 90 95

Asp Ala Tyr Glu Leu Lys Ile Ala Asn Lys Leu Phe Gly Glu Lys Thr

100 105 110

Tyr Gln Phe Leu Gln Glu Tyr Leu Asp Ala Ile Lys Lys Phe Tyr Gln
115 120 125

Thr Ser Val Glu Ser Thr Asp Phe Ala Asn Ala Pro Glu Glu Ser Arg
130 135 140

Lys Lys Ile Asn Ser Trp Val Glu Ser Gln Thr Asn Glu Lys Ile Lys
145 150 155 160

Asn Leu Phe Pro Asp Gly Thr Ile Gly Asn Asp Thr Thr Leu Val Leu
165 170 175

Val Asn Ala Ile Tyr Phe Lys Gly Gln Trp Glu Asn Lys Phe Lys Lys
180 185 190

Glu Asn Thr Lys Glu Glu Lys Phe Trp Pro Asn Lys Asn Thr Tyr Lys
195 200 205

Ser Val Gln Met Met Arg Gln Tyr Asn Ser Phe Asn Phe Ala Leu Leu
210 215 220

Glu Asp Val Gln Ala Lys Val Leu Glu Ile Pro Tyr Lys Gly Lys Asp
225 230 235 240

Leu Ser Met Ile Val Leu Leu Pro Asn Glu Ile Asp Gly Leu Gln Lys
245 250 255

Leu Glu Glu Lys Leu Thr Ala Glu Lys Leu Met Glu Trp Thr Ser Leu
260 265 270

Gln Asn Met Arg Glu Thr Cys Val Asp Leu His Leu Pro Arg Phe Lys
275 280 285

Met Glu Glu Ser Tyr Asp Leu Lys Asp Thr Leu Arg Thr Met Gly Met
290 295 300

Val Asn Ile Phe Asn Gly Asp Ala Asp Leu Ser Gly Met Thr Trp Ser
305 310 315 320

His Gly Leu Ser Val Ser Lys Val Leu His Lys Ala Phe Val Glu Val
325 330 335

Thr Glu Glu Gly Val Glu Ala Ala Ala Ala Thr Ala Val Val Val Val
340 345 350

Glu Leu Ser Ser Pro Ser Thr Asn Glu Glu Phe Cys Cys Asn His Pro
355 360 365

Phe Leu Phe Phe Ile Arg Gln Asn Lys Thr Asn Ser Ile Leu Phe Tyr
370 375 380

Gly Arg Phe Ser Ser Pro
385 390

<210> 11
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<213> Human

<400> 11
Met Glu Asp Leu Cys Val Ala Asn Thr Leu Phe Ala Leu Asn Leu Phe
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Lys His Leu Ala Lys Ala Ser Pro Thr Gln Asn Leu Phe Leu Ser Pro
20 25 30

Trp Ser Ile Ser Ser Thr Met Ala Met Val Tyr Met Gly Ser Arg Gly
35 40 45

Ser Thr Glu Asp Gln Met Ala Lys Val Leu Gln Phe Asn Glu Val Gly
50 55 60

Ala Asn Ala Val Thr Pro Met Thr Pro Glu Asn Phe Thr Ser Cys Gly
65 70 75 80

Phe Met Gln Gln Ile Gln Lys Gly Ser Tyr Pro Asp Ala Ile Leu Gln
85 90 95

Ala Gln Ala Ala Asp Lys Ile His Ser Ser Phe Arg Ser Leu Ser Ser
100 105 110

Ala Ile Asn Ala Ser Thr Gly Asp Tyr Leu Leu Glu Ser Val Asn Lys
115 120 125

Leu Phe Gly Glu Lys Ser Ala Ser Phe Arg Glu Glu Tyr Ile Arg Leu
130 135 140

Cys Gln Lys Tyr Tyr Ser Ser Glu Pro Gln Ala Val Asp Phe Leu Glu
145 150 155 160

Cys Ala Glu Glu Ala Arg Lys Ile Asn Ser Trp Val Lys Thr Gln
165 170 175

Thr Lys Gly Lys Ile Pro Asn Leu Leu Pro Glu Gly Ser Val Asp Gly
180 185 190

Asp Thr Arg Met Val Leu Val Asn Ala Val Tyr Phe Lys Gly Lys Trp
195 200 205

Lys Thr Pro Phe Glu Lys Lys Leu Asn Gly Leu Tyr Pro Phe Arg Val
210 215 220

Asn Ser Ala Gln Arg Thr Pro Val Gln Met Met Tyr Leu Arg Glu Lys
225 230 235 240

Leu Asn Ile Gly Tyr Ile Glu Asp Leu Lys Ala Gln Ile Leu Glu Leu
245 250 255

Pro Tyr Ala Gly Asp Val Ser Met Phe Leu Leu Leu Pro Asp Glu Ile
260 265 270

Ala Asp Val Ser Thr Gly Leu Glu Leu Glu Ser Glu Ile Thr Tyr
275 280 285

Asp Lys Leu Asn Lys Trp Thr Ser Lys Asp Lys Met Ala Glu Asp Glu
290 295 300

Val Glu Val Tyr Ile Pro Gln Phe Lys Leu Glu Glu His Tyr Glu Leu
305 310 315 320

Arg Ser Ile Leu Arg Ser Met Gly Met Glu Asp Ala Phe Asn Lys Gly
325 330 335

Arg Ala Asn Phe Ser Gly Met Ser Glu Arg Asn Asp Leu Phe Leu Ser
340 345 350

Glu Val Phe His Gln Ala Met Val Asp Val Asn Glu Glu Gly Thr Glu
355 360 365

Ala Ala Ala Gly Thr Gly Gly Val Met Thr Gly Arg Thr Gly His Gly
370 375 380

Gly Pro Gln Phe Val Ala Asp His Pro Phe Leu Phe Leu Ile Met His
385 390 395 400

Lys Ile Thr Lys Cys Ile Leu Phe Phe Gly Arg Phe Cys Ser Pro
405 410 415

<210> 12
<211> 8
<212> PRT
<213> Human

<400> 12
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1 5

<210> 13
<211> 9
<212> PRT
<213> Human

<400> 13
Val Arg Ile Lys Ala Glu Gly Lys Glu
1 5

<210> 14
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 14
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<210> 15
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic Primer

<400> 15
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<210> 16
<211> 405
<212> DNA
<213> Human

<400> 16
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tattttttctt ttcatttcctt aaggctttt gtctcaggcc ttctgagtag gagctggtgg 180
ccagcagtgt caaatagaaa gtgtttctca ctctccagca gctacagatg gatgtctact 240
ggggagcatt aaatagtatg ggtcagggtt attgagaaca actaatctta gaatgtttgg 300
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agaaatgggtt ggttatctatg gaccctttc ctggaaaaaa aaaaa 405

<210> 17
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic Peptide

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<221> PEPTIDE
<222> (3)
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<210> 18
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<212> DNA
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<400> 18
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cctgtgggca tcttgactgc aattggcatg gtcctcctgg ggacccgagg agccaccgct 180

ccccagttgg aggaggtgtt tcactctgaa aaagagacga agagctcaag aataaaggct 240
gaagaaaaag aggtgattga gaacacagaa gcagtagatc aacaattcca aaagttttg 300
actgaaataa gcaaactcac taatgattat gaactgaaca taaccaacag gctgtttgga 360
gaaaaaacat acctttccct tcaaaaatac ttagattatg ttgaaaaata ttatcatgca 420
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tgggttgaaa gcaaaacaaa tgaaaaatac aaggacttgt tcccagatgg ctctattagt 540
agctctacca agctggct ggtgaacatg gtttattta aaggcatacg ggacagggag 600
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gtacagatga tgacacagag ccattcctt agttcaactt 700

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<213> Human

<400> 19

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			20						25						30
Gly	Ile	Leu	Thr	Ala	Ile	Gly	Met	Val	Leu	Leu	Gly	Thr	Arg	Gly	Ala
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Thr	Ala	Ser	Gln	Leu	Glu	Glu	Val	Phe	His	Ser	Glu	Lys	Glu	Thr	Lys
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Ser	Ser	Arg	Ile	Lys	Ala	Glu	Glu	Lys	Glu	Val	Ile	Glu	Asn	Thr	Glu
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Ala	Val	His	Gln	Gln	Phe	Gln	Lys	Phe	Leu	Thr	Glu	Ile	Ser	Lys	Leu
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Thr	Asn	Asp	Tyr	Glu	Leu	Asn	Ile	Thr	Asn	Arg	Leu	Phe	Gly	Glu	Lys
							100					105			110
Thr	Tyr	Leu	Phe	Leu	Gln	Lys	Tyr	Leu	Asp	Tyr	Val	Glu	Lys	Tyr	Tyr
							115					120			125
His	Ala	Ser	Leu	Glu	Pro	Val	Asp	Phe	Val	Asn	Ala	Ala	Asp	Glu	Ser
							130					135			140
Arg	Lys	Lys	Ile	Asn	Ser	Trp	Val	Glu	Ser	Lys	Thr	Asn	Glu	Lys	Ile
							145					150			160
Lys	Asp	Leu	Phe	Pro	Asp	Gly	Ser	Ile	Ser	Ser	Ser	Thr	Lys	Leu	Val
							165					170			175
Leu	Val	Asn	Met	Val	Tyr	Phe	Lys	Gly	Gln	Trp	Asp	Arg	Glu	Phe	Lys
							180					185			190
Lys	Glu	Asn	Thr	Lys	Glu	Glu	Lys	Phe	Trp	Met	Asn	Lys	Ser	Thr	Ser
							195					200			205

Lys Ser Val Gln Met Met Thr Gln Ser His Ser Phe Ser Phe Thr Phe
210 215 220

<210> 20
<211> 478
<212> DNA
<213> Human

<400> 20

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gagcacaaag ccgactactc gggaatgtcg tcaggctccg gtttgcacgc ccagaagttc 219
ctgcacagtt cctttgtggc agtaactgag gaaggcaccg aggctgcacg tgccaccggc 279
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ctgttcttca tcaggcacaa tgaatccaac agcatcctct tcttcggcag attttcttct 399
ccttaagatg atcgttgcca tggcattgct gcttttagca aaaaacaact accagtggta 459
ctcatatgaa tatgaaaat 478

<210> 21
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<212> PRT
<213> Homo sapiens

<400> 21

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Pro Gly His Met Glu Glu Arg Lys Val Asn Leu His Leu Pro Arg Phe
20 25 30

Glu Val Glu Asp Ser Tyr Asp Leu Glu Ala Val Leu Ala Ala Met Gly
35 40 45

Met Gly Asp Ala Phe Ser Glu His Lys Ala Asp Tyr Ser Gly Met Ser
50 55 60

Ser Gly Ser Gly Leu Tyr Ala Gln Lys Phe Leu His Ser Ser Phe Val
65 70 75 80

Ala Val Thr Glu Glu Gly Thr Glu Ala Ala Ala Ala Thr Gly Ile Gly
85 90 95

Phe Thr Val Thr Ser Ala Pro Gly His Glu Asn Val His Cys Asn His
100 105 110

Pro Phe Leu Phe Phe Ile Arg His Asn Glu Ser Asn Ser Ile Leu Phe
115 120 125

Phe Gly Arg Phe Ser Ser Pro
130 135